

08/484, 346  
12/5/96

SYSTEM:OS - DIALOG OneSearch

File 55:BIOSIS PREVIEWS(R) 1985-1996/Nov W4  
(c) 1996 BIOSIS

File 72:EMBASE 1985-1996/Iss 48  
(c) 1996 Elsevier Science B.V.

File 76:Life Sciences Collection 1982-1996/Oct  
(c) 1996 Cambridge Sci Abs

File 155:MEDLINE(R) 1966-1996/Dec W4  
(c) format only 1996 Knight-Ridder Info

\*File 155: MEDLINE updates delayed. See HELP DELAY 155.

File 342:Derwent Patents Citation Indx 1978-96/96C46  
(c) 1996 Derwent Info Ltd

File 348:EUROPEAN PATENTS 1978-1996/Nov W4  
(c) 1996 European Patent Office

\*File 348: \*\*\* EPO is now CURRENT! \*\*\*

Fulltext is forthcoming. See HELP NEWS 348 for more information.

File 399:CA SEARCH(R) 1967-1996/UD=12524  
(c) 1996 American Chemical Society

\*File 399: Use is subject to the terms of your user/customer agreement.  
For format prices, including formats 6 & 8, see HELP RATES 399.

Set Items Description

--- -----

?E AU=SMITH, LLO

Ref	Items	Index-term
E1	1	AU=SMITH, LISA MARIE
E2	1	AU=SMITH, LISA MARLENE J.
E3	0	*AU=SMITH, LLO
E4	8	AU=SMITH, LLOYD
E5	2	AU=SMITH, LLOYD D.
E6	8	AU=SMITH, LLOYD H.
E7	14	AU=SMITH, LLOYD H., JR.
E8	1	AU=SMITH, LLOYD HERBERT
E9	8	AU=SMITH, LLOYD HOLLINGWORTH, JR.
E10	1	AU=SMITH, LLOYD L.
E11	34	AU=SMITH, LLOYD L., JR.
E12	4	AU=SMITH, LLOYD LYMAN, JR.

Enter P or PAGE for more

?P

Ref Items Index-term

E13	84	AU=SMITH, LLOYD M.
E14	1	AU=SMITH, LLOYD MARK
E15	1	AU=SMITH, LLOYD MICHAEL
E16	6	AU=SMITH, LLOYD MUIR
E17	9	AU=SMITH, LLOYD R.
E18	1	AU=SMITH, LLOYD V.
E19	1	AU=SMITH, LLOYD, M.
E20	1	AU=SMITH, LOIS
E21	3	AU=SMITH, LOIS E. H.
E22	1	AU=SMITH, LOIS ELAINE H.
E23	1	AU=SMITH, LOIS ELAINE HODGSON
E24	1	AU=SMITH, LOIS JEAN

Enter P or PAGE for more

?S E13

S1        84    AU="SMITH, LLOYD M."  
 ?E AU=HOOD, L

Ref	Items	Index-term
E1	7	AU=HOOD, KEVIN
E2	0	*AU=HOOD, L
E3	229	AU=HOOD, L.
E4	1	AU=HOOD, L. DAVID
E5	14	AU=HOOD, L. E.
E6	29	AU=HOOD, L. F.
E7	19	AU=HOOD, L. L.
E8	2	AU=HOOD, L. M.
E9	1	AU=HOOD, L. R.
E10	4	AU=HOOD, L. V. S.
E11	1	AU=HOOD, L.C.
E12	78	AU=HOOD, L.E.

Enter P or PAGE for more

?P

Ref	Items	Index-term
E13	1	AU=HOOD, L.F.
E14	4	AU=HOOD, L.J.
E15	1	AU=HOOD, L.L.
E16	1	AU=HOOD, L.V.S.
E17	1	AU=HOOD, L,
E18	12	AU=HOOD, LAMARTINE F.
E19	11	AU=HOOD, LAMARTINE F. (ED)
E20	4	AU=HOOD, LARRY H.

E21	1	AU=HOOD, LARRY HUDSON
E22	8	AU=HOOD, LARRY L.
E23	1	AU=HOOD, LARRY R.
E24	6	AU=HOOD, LEE

Enter P or PAGE for more

?P

Ref	Items	Index-term
E25	271	AU=HOOD, LEROY
E26	147	AU=HOOD, LEROY E.
E27	1	AU=HOOD, LINDSAY M.
E28	3	AU=HOOD, LON L.
E29	1	AU=HOOD, LORETTA L.
E30	1	AU=HOOD, LYAL V.
E31	5	AU=HOOD, LYAL V. S.
E32	1	AU=HOOD, LYDIA CHEN
E33	5	AU=HOOD, M.
E34	5	AU=HOOD, M. A.
E35	2	AU=HOOD, M. B.
E36	2	AU=HOOD, M. J.

Enter P or PAGE for more

?S E25 OR E26

	271	AU=HOOD, LEROY
	147	AU=HOOD, LEROY E.
S2	418	AU="HOOD, LEROY" OR AU="HOOD, LEROY E."

?RD

>>>Duplicate detection is not supported for File 342.

>>>Duplicate detection is not supported for File 348.

>>>Records from unsupported files will be retained in the RD set.

...examined 50 records (50)

...examined 50 records (100)

...examined 50 records (150)

...examined 50 records (200)

...examined 50 records (250)

...examined 50 records (300)

...examined 50 records (350)

...examined 50 records (400)

...completed examining records

S3	411	RD (unique items)
----	-----	-------------------

?E AU=HUNKAPILLER, T

Ref	Items	Index-term
E1	73	AU=HUNKAPILLER, MICHAEL W.
E2	1	AU=HUNKAPILLER, MIKE
E3	0	*AU=HUNKAPILLER, T
E4	19	AU=HUNKAPILLER, T.
E5	24	AU=HUNKAPILLER, TIM
E6	2	AU=HUNKAPILLER, TIM J.
E7	1	AU=HUNKAPILLER, TIM.
E8	2	AU=HUNKAR D
E9	2	AU=HUNKAR D B
E10	1	AU=HUNKAR DB
E11	1	AU=HUNKAR DE
E12	1	AU=HUNKAR K

Enter P or PAGE for more

?S E5 OR E6 OR E7

	24	AU=HUNKAPILLER, TIM
	2	AU=HUNKAPILLER, TIM J.
	1	AU=HUNKAPILLER, TIM.
S4	27	AU="HUNKAPILLER, TIM" OR AU="HUNKAPILLER, TIM J." OR AU="HUNKAPILLER, TIM."

?E AU=HUNKAPILLER, M

Ref	Items	Index-term
E1	15	AU=HUNKAPILLER T.
E2	1	AU=HUNKAPILLER TJ
E3	0	*AU=HUNKAPILLER, M
E4	12	AU=HUNKAPILLER, M.
E5	13	AU=HUNKAPILLER, M. W.
E6	34	AU=HUNKAPILLER, M.W.
E7	11	AU=HUNKAPILLER, MICHAEL
E8	73	AU=HUNKAPILLER, MICHAEL W.
E9	1	AU=HUNKAPILLER, MIKE
E10	19	AU=HUNKAPILLER, T.
E11	24	AU=HUNKAPILLER, TIM
E12	2	AU=HUNKAPILLER, TIM J.

Enter P or PAGE for more

?S E8

S5	73	AU="HUNKAPILLER, MICHAEL W."
----	----	------------------------------

?E AU=CONNELL, C

Ref	Items	Index-term
E1	1	AU=CONNELL, BARRY
E2	1	AU=CONNELL, BRIAN T.
E3	0	*AU=CONNELL, C
E4	4	AU=CONNELL, C.
E5	2	AU=CONNELL, C. L.
E6	1	AU=CONNELL, C.D.
E7	5	AU=CONNELL, C.R.
E8	3	AU=CONNELL, CAROLYN J.
E9	1	AU=CONNELL, CAROLYN J. A.
E10	1	AU=CONNELL, CATHERINE M.
E11	5	AU=CONNELL, CECIL H.
E12	1	AU=CONNELL, CHARLES

Enter P or PAGE for more

?P

Ref	Items	Index-term
E13	15	AU=CONNELL, CHARLES R.
E14	1	AU=CONNELL, CHARLES ROBERT
E15	1	AU=CONNELL, CHRIS
E16	4	AU=CONNELL, D.
E17	1	AU=CONNELL, D. C.
E18	1	AU=CONNELL, D. E.
E19	1	AU=CONNELL, D. I.
E20	2	AU=CONNELL, D. J.
E21	3	AU=CONNELL, D. L.
E22	2	AU=CONNELL, D. R.
E23	48	AU=CONNELL, D. W.
E24	64	AU=CONNELL, D.W.

Enter P or PAGE for more

?S E13

S6	15	AU="CONNELL, CHARLES R."
----	----	--------------------------

?DS

Set	Items	Description
S1	84	AU="SMITH, LLOYD M."
S2	418	AU="HOOD, LEROY" OR AU="HOOD, LEROY E."
S3	411	RD (unique items)
S4	27	AU="HUNKAPILLER, TIM" OR AU="HUNKAPILLER, TIM J." OR AU="H-UNKAPILLER, TIM."
S5	73	AU="HUNKAPILLER, MICHAEL W."
S6	15	AU="CONNELL, CHARLES R."

?S S1 OR S3 OR S4 OR S5 OR S6

84 S1

411 S3

27 S4

73 S5

15 S6

S7 551 S1 OR S3 OR S4 OR S5 OR S6

?RD

>>>Duplicate detection is not supported for File 342.

>>>Duplicate detection is not supported for File 348.

>>>Records from unsupported files will be retained in the RD set.

...examined 50 records (50)

...examined 50 records (100)

...examined 50 records (150)

...examined 50 records (200)

...examined 50 records (250)

...examined 50 records (300)

...examined 50 records (350)

...examined 50 records (400)

...examined 50 records (450)

...examined 50 records (500)

...examined 50 records (550)

...completed examining records

S8 547 RD (unique items)

?S FLUORESC? (3N) (PRIMER# OR OLIGONUCLEOTIDE# OR POLYNUCLEOTIDE#)

503022 FLUORESC?

0 PRIMER#

0 OLIGONUCLEOTIDE#

0 POLYNUCLEOTIDE#

S9 0 FLUORESC? (3N) (PRIMER# OR OLIGONUCLEOTIDE# OR  
POLYNUCLEOTIDE#)

?S FLUORESC? (3N) (PRIMER? OR OLIGONUCLEOTIDE? OR POLYNUCLEOTIDE?)

Processing

503022 FLUORESC?

91955 PRIMER?

89864 OLIGONUCLEOTIDE?

17674 POLYNUCLEOTIDE?

S10 1902 FLUORESC? (3N) (PRIMER? OR OLIGONUCLEOTIDE? OR  
POLYNUCLEOTIDE?)

?S S8 AND S10

547 S8

1902 S10  
S11 13 S8 AND S10  
?T'S11/3,AB/1-13

>>>No matching display code(s) found in file(s): 342, 399

11/3,AB/1 (Item 1 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

123277020 CA: 123(21)277020j JOURNAL  
DMSO resolves certain compressions and signal dropouts in fluorescent dye  
labeled primer-based DNA sequencing reactions  
AUTHOR(S): Seto, Donald; Seto, Jason; Deshpande, Purnima; Hood, Leroy  
LOCATION: Div. Biology, California Inst. Technology, Pasadena, CA, 91125,  
USA  
JOURNAL: DNA Sequence DATE: 1995 VOLUME: 5 NUMBER: 3 PAGES: 131-40  
CODEN: DNSEES ISSN: 1042-5179 LANGUAGE: English

11/3,AB/2 (Item 2 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

122152589 CA: 122(13)152589z JOURNAL  
Direct fluorescence analysis of genetic polymorphisms by hybridization  
with oligonucleotide arrays on glass supports  
AUTHOR(S): Guo, Zhen; Guilfoyle, Richard A.; Thiel, Andrew J.; Wang,  
Renfeng; Smith, Lloyd M.  
LOCATION: Dep. Chemistry, Univ. Wisconsin, Madison, WI, 53706-1396, USA  
JOURNAL: Nucleic Acids Res. DATE: 1994 VOLUME: 22 NUMBER: 24 PAGES:  
5456-65 CODEN: NARHAD ISSN: 0305-1048 LANGUAGE: English

11/3,AB/3 (Item 3 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

120046795 CA: 120(5)46795n JOURNAL  
Fluorescence-based DNA sequencing with hexamer primers. (Erratum to  
document cited in CA119(17):174885h)  
AUTHOR(S): Hou, Weiying; Smith, Lloyd M.  
LOCATION: Dep. Chem., Univ. Wisconsin, Madison, WI, 53706, USA  
JOURNAL: Nucleic Acids Res. DATE: 1993 VOLUME: 21 NUMBER: 17 PAGES:  
4158 CODEN: NARHAD ISSN: 0305-1048 LANGUAGE: English

11/3,AB/4 (Item 4 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

119110012 CA: 119(11)110012p JOURNAL  
Specific primer-directed DNA sequence analysis using automated  
fluorescence detection and labeled primers  
AUTHOR(S): Kaiser, Robert; Hunkapiller, Tim; Heiner, Cheryl; Hood, Leroy  
LOCATION: Sch. Med., Univ. Washington, Seattle, WA, 98195, USA  
JOURNAL: Methods Enzymol. DATE: 1993 VOLUME: 218 NUMBER: Recombinant  
DNA, Pt. I PAGES: 122-53 CODEN: MENZAU ISSN: 0076-6879 LANGUAGE:  
English

11/3,AB/5 (Item 5 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

115227794 CA: 115(21)227794d PATENT  
4,7-Dichlorofluorescein dyes as molecular probes, their preparation, and  
their use in DNA sequencing  
INVENTOR(AUTHOR): Menchen, Steven M.; Lee, Linda G.; Connell, Charles R.;  
Hershey, N. Davis; Chakerian, Vergine; Woo, Sam Lee; Fung, Steven  
LOCATION: USA  
ASSIGNEE: Applied Biosystems, Inc.  
PATENT: PCT International ; WO 9107507 A1 DATE: 910530  
APPLICATION: WO 90US6608 (901113) \*US 436455 (891114)  
PAGES: 39 pp. CODEN: PIXXDZ LANGUAGE: English CLASS: C12Q-001/68A;  
C07H-017/00B; C07D-311/82B; C07D-311/90B DESIGNATED COUNTRIES: JP  
DESIGNATED REGIONAL: AT; BE; CH; DE; DK; ES; FR; GB; GR; IT; LU; NL; SE

11/3,AB/6 (Item 6 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

112217467 CA: 112(23)217467y PATENT  
Preparation of 2'- or 5'-aminodeoxynucleoside phosphoramidites and their  
use for the preparation of oligonucleotides having aliphatic amino groups  
INVENTOR(AUTHOR): Smith, Lloyd M.; Fung, Steven  
LOCATION: USA  
ASSIGNEE: California Institute of Technology  
PATENT: United States ; US 4849513 A DATE: 890718  
APPLICATION: US 878045 (860624) \*US 565010 (831220) \*US 709579 (850308)  
PAGES: 30 pp. Cont.-in-part of U.S. Ser. No. 565,010, abandoned. CODEN:  
USXXAM LANGUAGE: English CLASS: 536027000; C07H-019/10A; C07H-019/20B



11/3,AB/7 (Item 7 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

111147979 CA: 111(17)147979v JOURNAL  
Specific-primer-directed DNA sequencing using automated fluorescence  
detection  
AUTHOR(S): Kaiser, Robert J.; MacKellar, Sara L.; Vinayak, Ravi S.;  
Sanders, Jane Z.; Saavedra, Raul A.; Hood, Leroy E.  
LOCATION: Div. Biol., California Inst. Technol., Pasadena, CA, 91125, USA  
JOURNAL: Nucleic Acids Res. DATE: 1989 VOLUME: 17 NUMBER: 15 PAGES:  
6087-102 CODEN: NARHAD ISSN: 0305-1048 LANGUAGE: English

11/3,AB/8 (Item 8 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

110208962 CA: 110(23)208962n PATENT  
Amino-derivatized phosphite and phosphate linking agents, phosphoramidite  
precursors, and useful conjugates  
INVENTOR(AUTHOR): Fung, Steven; Woo, Sam Lee; Smith, Lloyd M.  
LOCATION: USA  
ASSIGNEE: Applied Biosystems, Inc.  
PATENT: PCT International ; WO 8802004 A1 DATE: 880324  
APPLICATION: WO 86US1970 (860920)  
PAGES: 41 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C07F-009/22A;  
C07F-009/24B; C07H-019/10B; C07H-019/20B DESIGNATED COUNTRIES: AU; JP  
DESIGNATED REGIONAL: AT; BE; CH; DE; FR; GB; IT; LU; NL; SE

11/3,AB/9 (Item 9 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

110075990 CA: 110(9)75990w PATENT  
Preparation of aminodeoxyribonucleoside phosphoramidites and their use  
for the preparation of fluorescent-labeled oligonucleotides  
INVENTOR(AUTHOR): Smith, Lloyd M.; Fung, Steven; Kaiser, Robert J., Jr.  
LOCATION: USA  
ASSIGNEE: California Institute of Technology  
PATENT: PCT International ; WO 8800201 A1 DATE: 880114  
APPLICATION: WO 87US1422 (870622) \*US 878045 (860624)  
PAGES: 106 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C07H-019/06A;  
C07H-019/067B; C07H-019/073B; C07H-019/16B; C07H-019/167B; C07H-019/173B;  
C07H-021/00B; C07H-021/02B; C07H-021/04B DESIGNATED COUNTRIES: JP

DESIGNATED REGIONAL: AT; BE; CH; DE; FR; GB; IT; LU; NL; SE

11/3,AB/10 (Item 10 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

110024247 CA: 110(3)24247b PATENT  
Preparation of 2-substituted-3-protected 1,3,2-oxazaphosphacycloalkanes,  
their phosphoramidite precursors, and their use for introducing spacer  
groups of labeled oligonucleotides by solid phase method  
INVENTOR(AUTHOR): Fung, Steven; Woo, Sam L.; Smith, Lloyd M.  
LOCATION: USA  
ASSIGNEE: Applied Biosystems, Inc.  
PATENT: United States ; US 4757141 A DATE: 880712  
APPLICATION: US 769170 (850826)  
PAGES: 7 pp. CODEN: USXXAM LANGUAGE: English CLASS: 536027000;  
C07H-019/06A; C07H-019/10B; C07H-019/16B; C07H-019/20B

11/3,AB/11 (Item 11 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

108199454 CA: 108(23)199454c JOURNAL  
The synthesis and use of fluorescent oligonucleotides in DNA sequence  
analysis  
AUTHOR(S): Smith, Lloyd M.; Kaiser, Robert J.; Sanders, Jane Z.; Hood,  
Leroy E.  
LOCATION: Div. Biol., California Inst Technol., Pasadena, CA, 91125, USA  
JOURNAL: Methods Enzymol. DATE: 1987 VOLUME: 155 NUMBER: Recomb. DNA,  
Pt. F PAGES: 260-301 CODEN: MENZAU ISSN: 0076-6879 LANGUAGE: English

11/3,AB/12 (Item 12 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
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108128114 CA: 108(15)128114f PATENT  
Method of detecting electrophoretically separated oligonucleotides  
INVENTOR(AUTHOR): Fung, Steven; Woo, Sam Lee; Menchen, Steven M.;  
Connell, Charles R.; Heiner, Cheryl  
LOCATION: USA  
ASSIGNEE: Applied Biosystems, Inc.  
PATENT: European Pat. Appl. ; EP 233053 A2 DATE: 870819  
APPLICATION: EP 87300998 (870204) \*US 827348 (860207)  
PAGES: 30 pp. CODEN: EPXXDW LANGUAGE: English CLASS: C12Q-001/68A;

G01N-033/58B; C07H-021/00 DESIGNATED COUNTRIES: AT; BE; CH; DE; ES; FR; GB  
; GR; IT; LI; LU; NL; SE

11/3,AB/13 (Item 13 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

103178571 CA: 103(21)178571v JOURNAL

The synthesis of oligonucleotides containing an aliphatic amino group at  
the 5' terminus: synthesis of fluorescent DNA primers for use in DNA  
sequence analysis

AUTHOR(S): Smith, Lloyd M.; Fung, Steven; Hunkapiller, Michael W.;  
Hunkapiller, Tim J.; Hood, Leroy E.

LOCATION: Div. Biol., California Inst. Technol., Pasadena, CA, 91125, USA

JOURNAL: Nucleic Acids Res. DATE: 1985 VOLUME: 13 NUMBER: 7 PAGES:  
2399-412 CODEN: NARHAD ISSN: 0305-1048 LANGUAGE: English  
?DS

Set	Items	Description
S1	84	AU="SMITH, LLOYD M."
S2	418	AU="HOOD, LEROY" OR AU="HOOD, LEROY E."
S3	411	RD (unique items)
S4	27	AU="HUNKAPILLER, TIM" OR AU="HUNKAPILLER, TIM J." OR AU="H- UNKAPILLER, TIM."
S5	73	AU="HUNKAPILLER, MICHAEL W."
S6	15	AU="CONNELL, CHARLES R."
S7	551	S1 OR S3 OR S4 OR S5 OR S6
S8	547	RD (unique items)
S9	0	FLUORESC? (3N) (PRIMER# OR OLIGONUCLEOTIDE# OR POLYNUCLEOT- IDE#)
S10	1902	FLUORESC? (3N) (PRIMER? OR OLIGONUCLEOTIDE? OR POLYNUCLEOT- IDE?)
S11	13	S8 AND S10

?S S10 NOT PY>1984

Processing  
Processing  
Processing  
Processing  
Processing  
Processing  
Processing

1902 S10  
24168754 PY>1984  
S12 105 S10 NOT PY>1984

?RD

>>>Duplicate detection is not supported for File 342.

>>>Duplicate detection is not supported for File 348.

>>>Records from unsupported files will be retained in the RD set.

...examined 50 records (50)

...examined 50 records (100)

...completed examining records

S13 93 RD (unique items)

?S SEQUENC? OR ELECTROPHORESIS OR DETECT?

Processing

Processing

Processing

1149183 SEQUENC?

358447 ELECTROPHORESIS

1597150 DETECT?

S14 2849976 SEQUENC? OR ELECTROPHORESIS OR DETECT?

?S 13 AND S14

Processing

757917 13

2849976 S14

S15 123850 13 AND S14

?S S13 AND S14

93 S13

2849976 S14

S16 19 S13 AND S14

?T S16/3,AB/1-19

>>>No matching display code(s) found in file(s): 342, 399

16/3,AB/1 (Item 1 from file: 76)

DIALOG(R)File 76:Life Sciences Collection

(c) 1996 Cambridge Sci Abs. All rts. reserv.

00588461 0333095

Thin-Layer Chromatography of Oligonucleotides: A Device to Aid the  
Ultraviolet Detection of Fingerprint Patterns.

Steinhaeuser, K.; Woolley, P.

Max-Planck-Inst. Mol. Genet. (Abteil. Wittmann), Ihnestr. 63, 1000 Berlin  
33, FRG

ANAL. BIOCHEM. vol. 120, no. 1, pp. 189-192 (1982.)

DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH

SUBFILE: Biochemistry Abstracts Part 2: Nucleic Acids

The observation by uv light of thin-layer fingerprint chromatograms of oligonucleotides is impeded by the use of acid eluents. A simple device is described which overcomes this difficulty.

16/3,AB/2 (Item 1 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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05440797 85056797

A rapid procedure for visualising the inner cell mass and trophectoderm nuclei of mouse blastocysts in situ using polynucleotide-specific fluorochromes.

Handyside AH; Hunter S

J Exp Zool (UNITED STATES) Sep 1984, 231 (3) p429-34, ISSN 0022-104X  
Journal Code: I47

Languages: ENGLISH

Document type: JOURNAL ARTICLE

A rapid procedure has been devised to count the numbers of outer trophectoderm (TE) and inner cell mass (ICM) cells of mouse blastocysts by differentially labelling their nuclei in situ with polynucleotide-specific fluorochromes. The TE nuclei were labelled with propidium iodide (PI) by permeabilising the cells using selective antibody-mediated complement lysis (Solter and Knowles, '75). The blastocysts were then fixed in ethanol and the ICM nuclei labelled with bisbenzimidazole. These two fluorochromes have widely different fluorescent spectra. Thus, by using fluorescence microscopy with appropriate filter combinations, the PI-labelled TE nuclei appeared pink or red; the bisbenzimidazole-labelled ICM nuclei, blue or unlabelled. The total numbers of blastocyst nuclei and the numbers of ICM nuclei counted by differential labelling were similar to the numbers detected after spreading the nuclei of intact blastocysts or immunosurgically isolated ICMs by air-drying (Tarkowski '66). Differential labelling of TE and ICM nuclei in situ has two important advantages--that the numbers of both these cell types can be determined for individual blastocysts and that spatial relationships are partially preserved so that regional interactions can be studied.

16/3,AB/3 (Item 2 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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04685550 82228550

Thin-layer chromatography of oligonucleotides: a device to aid the ultraviolet detection of fingerprint patterns.

Steinhauser L; Woolley P; Friedrich K

Anal Biochem (UNITED STATES) Feb 1982, 120 (1) p189-92, ISSN  
0003-2697 Journal Code: 4NK  
Languages: ENGLISH  
Document type: JOURNAL ARTICLE

16/3,AB/4 (Item 3 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
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04570896 82113896

Fluorescence-determined preferential binding of quinacrine to DNA.  
Baldini G; Doglia S; Dolci S; Sassi G  
Biophys J (UNITED STATES) Dec 1981, 36 (3) p465-77, ISSN 0006-3495  
Journal Code: A5S  
Languages: ENGLISH  
Document type: JOURNAL ARTICLE

Quinacrine complexes with native DNA (Calf thymus, *Micrococcus lysodeikticus*, *Escherichia coli*, *Bacillus subtilis*, and *Colstridium perfringens*) and synthetic polynucleotides (poly(dA) . poly(dT), poly[d(A-T)] . poly[d(A-T)], poly(dG) . poly(dC) and poly[d(G-C)] . poly[d(G-C)]) has been investigated in solution at 0.1 M NaCl, 0.05 M Tris HCl, 0.001 M EDTA, pH 7.5, at 20 degrees C. Fluorescence excitation spectra of complexes with dye concentration  $D = 5-30$  microM and DNA phosphate concentration  $P = 400$  microM have been examined from 300 to 500 nm, while collecting the emission above 520 nm. The amounts of free and bound quinacrine in the dye-DNA complexes have been determined by means of equilibrium dialysis experiments. Different affinities have been found for the various DNAs and their values have been examined with a model that assumes that the binding constants associated with alternating purine and pyrimidine sequences are larger than those relative to nonalternating ones. Among the alternating nearest neighbor base sequences, the Pyr(3'-5')Pur sequences, i.e., C-G, T-G, C-A and T-A seem to bind quinacrine stronger than the remaining sequences. In particular the three sites, where a G . C base pair is involved, are found to display higher affinities. Good agreement is found with recent calculations on the energetics of intercalation sites in DNA. The analysis of the equilibrium shows also that the strength of the excitation spectrum of bound dye depends strongly upon the ratio of bound quinacrine to DNA. This effect can be attributed to dye-dye energy transfer along DNA.

16/3,AB/5 (Item 4 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
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04134574 80245574

Energy transfer and binding competition between dyes used to enhance staining differentiation in metaphase chromosomes.

Sahar E; Latt SA

Chromosoma (GERMANY, WEST) 1980, 79 (1) p1-28, ISSN 0009-5915

Journal Code: D7A

Languages: ENGLISH

Document type: JOURNAL ARTICLE; REVIEW

The ability of electronic energy transfer and direct binding competition between pairs of dyes to enhance contrast in human or bovine metaphase chromosome staining patterns is illustrated, and the relative effectiveness of these two mechanisms compared. The existence of energy transfer between quinacrine or 33258 Hoechst and 7-amino-actinomycin D in doubly stained chromosomes is demonstrated directly by microfluorometry. The ability of the dyes 7-amino-actinomycin D, methyl green, or netropsin, acting as counterstains, to displace quinacrine, 33258 Hoechst, or chromomycin A3 from chromosomes, is estimated by quantitative analysis of energy transfer data, by photobleaching of the counterstains, or by selective removal of counterstains by appropriate synthetic polynucleotides. Effects on the fluorescence of soluble 33258 Hoechst-DNA complexes due to energy transfer or binding displacement, by actinomycin D or netropsin, respectively, are further differentiated by nanosecond fluorescence decay measurements. Examples are presented of dye combinations for which (a) energy transfer is the primary mechanism operative, (b) binding competition exists, with consequences reinforcing those due to energy transfer, or (c) binding competition is the most important interaction. These analyses of mechanisms responsible for contrast enhancement in doubly stained chromosomes are used to derive information about the relationship between chromosome composition and banding patterns.

16/3,AB/6 (Item 5 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

(c) format only 1996 Knight-Ridder Info. All rts. reserv.

03532198 78166198

Interaction of phenosafranine with nucleic acids and model polyphosphates. I. Self-aggregation and complex formation with inorganic polyphosphates.

Balcarova TZ; Kleinwachter V; Koudelka J

Biophys Chem (NETHERLANDS) Mar 1978, 8 (1) p17-25, ISSN 0301-4622

Journal Code: A5T

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Aggregation of phenosafranine in concentrated aqueous solutions and interaction with polyphosphates was studied by absorption and fluorescence spectroscopy. At concentrations greater than  $10^{-3}$  M phenosafranine forms dimers ( $K_d = 3.8 \times 10^2$  l.mole $^{-1}$ ), which are characterized by a

hypsochromic shift of the visible and near ultraviolet absorption maxima accompanied by a hypochromic effect. No fluorescence could be detected from phenosafranine dimers. Analogous spectra changes were observed when a polyphosphate was titrated with phenosafranine, which indicated that with increasing saturation of the polyphosphate binding sites phenosafranine gradually became bound in the aggregated form. Full saturation of the polyphosphate binding sites with phenosafranine was reached only when an excess of free dye was present. The cooperative binding of phenosafranine to a polyphosphate could be evaluated by means of a theory proposed by Schwarz et al. At the zero ionic strength and at 25 degrees C the binding was characterized by cooperative binding constant  $K = 6.2 \times 10^5 \text{ l.mole}^{-1}$ , number of binding sites per monomeric phosphate residue  $g = 0.4$ , and cooperativity parameter  $q=30$ . Spectroscopic properties of phenosafranine in the aggregated and polyphosphate-bound states were compared with those of ethidium bromide.

16/3,AB/7 (Item 6 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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03419002 78053002

Analysis of single- and double-stranded nucleic acids on polyacrylamide and agarose gels by using glyoxal and acridine orange.

McMaster GK; Carmichael GG

Proc Natl Acad Sci U S A (UNITED STATES) Nov 1977, 74 (11) p4835-8,

ISSN 0027-8424 Journal Code: PV3

Languages: ENGLISH

Document type: JOURNAL ARTICLE

We have developed a simple and rapid system for the denaturation of nucleic acids and their subsequent analysis by gel electrophoresis. RNA and DNA are denatured in 1 M glyoxal (ethanedial) and 50% (vol/vol) dimethyl sulfoxide, at 50 degrees. The glyoxalated nucleic acids are then subjected to electrophoresis through either acrylamide or agarose gels in a 10 mM sodium phosphate buffer at pH 7.0. When glyoxalated DNA molecules of known molecular weights are used as standards, accurate molecular weights for RNA are obtained. Furthermore, we have employed the metachromatic stain acridine orange for visualization of nucleic acids in gels. This dye interacts differently with double- and single-stranded polynucleotides, fluorescing green and red, respectively. By using these techniques, native and denatured DNA and RNA molecules can be analyzed on the same slab gel.

16/3,AB/8 (Item 7 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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03259600 77161600

Optical Studies of the interaction of 4'-6'-diamidino-2-phenylindole with DNA and metaphase chromosomes.

Lin MS; Comings DE; Alfi OS

Chromosoma (GERMANY, WEST) Mar 7 1977, 60 (1) p15-25, ISSN 0009-5915  
Journal Code: D7A

Languages: ENGLISH

Document type: JOURNAL ARTICLE

The optical absorption and fluorescence characteristics of 4'-6'-diamidino-2-phenylindole (DAPI) with DNA and chromosomes were studied. There is a decrease in extinction coefficient and shift in the absorption spectra to a higher wavelength when the dye binds to DNA. The fluorescence of DAPI is enhanced by both A-T and G-C base-pairs. The enhancement by A-T rich is significantly greater than by G-C rich DNA. The chromosomes and the constrictions of human chromosomes 1 and 16; these regions are known to contain A-T rich DNA and show dull fluorescence when treated with quinacrine. This dye may be useful for identifying A-T rich region in chromosomes. The fluorescence of DAPI bound to polynucleotides or chromosomes is partially quenched by the introduction of BrdU. This suppression of dye fluorescence allows optical detection of sister chromatid exchanges and chromosome region containing DNA with an unequal distribution of thymidine between polynucleotide chains after BrdU incorporation.

16/3,AB/9 (Item 8 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

(c) format only 1996 Knight-Ridder Info. All rts. reserv.

02872034 76053034

DNA polyintercalating drugs: DNA binding of diacridine derivatives.

Le Pecq JB; Le Bret M; Barbet J; Roques B

Proc Natl Acad Sci U S A (UNITED STATES) Aug 1975, 72 (8) p2915-9,  
ISSN 0027-8424 Journal Code: PV3

Languages: ENGLISH

Document type: JOURNAL ARTICLE

As a first step in the synthesis and the study of DNA polyintercalating drugs, dimers of acridines have been prepared. Their DNA binding properties have been studied. It has been determined that when the chain separating the two aromatic rings is longer than a critical distance, bisintercalation is actually observed and that the DNA binding affinity becomes quite large (greater than  $10^{(8)}-10^{(9)}$  M<sup>-1</sup>). It is shown also that the optical characteristics of these molecules are dependent on the sequences of DNA. The fluorescence intensity of one of these dimers when bound to DNA varies as the fourth power of its A+T content. This derivative could be used as a fluorescent probe of DNA sequence.

16/3,AB/10 (Item 9 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
(c) format only 1996 Knight-Ridder Info. All rts. reserv.

02685913 75092913  
Optical studies of complexes of quinacrine with DNA and chromatin:  
implications for the fluorescence of cytological chromosome preparations.  
Latt SA; Brodie S; Munroe SH  
Chromosoma (GERMANY, WEST) 1974, 49 (1) p17-40, ISSN 0009-5915  
Journal Code: D7A  
Languages: ENGLISH  
Document type: JOURNAL ARTICLE

16/3,AB/11 (Item 10 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
(c) format only 1996 Knight-Ridder Info. All rts. reserv.

02456458 74174458  
Fluorescent probes of chromosomal DNA structure: three classes of  
acridines.  
Weisblum B  
Cold Spring Harb Symp Quant Biol (UNITED STATES) 1974, 38 p441-9,  
ISSN 0091-7451 Journal Code: DMT  
Languages: ENGLISH  
Document type: JOURNAL ARTICLE

16/3,AB/12 (Item 11 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
(c) format only 1996 Knight-Ridder Info. All rts. reserv.

02251497 73230497  
Chemical post-labeling methods for the base composition and sequence  
analysis of RNA.  
Randerath K; Randerath E  
J Chromatogr (NETHERLANDS) Jul 18 1973, 82 (1) p59-74, ISSN 0021-9673  
Journal Code: HQF  
Languages: ENGLISH  
Document type: JOURNAL ARTICLE

16/3,AB/13 (Item 12 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
(c) format only 1996 Knight-Ridder Info. All rts. reserv.

01966237 72216237

Quantum yield of acridines interacting with DNA of defined sequence. A basis for the explanation of acridine bands in chromosomes.

Pachmann U; Rigler R

Exp Cell Res (UNITED STATES) Jun 1972, 72 (2) p602-8, ISSN 0014-4827

Journal Code: EPB

Languages: ENGLISH

Document type: JOURNAL ARTICLE

16/3,AB/14 (Item 13 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

(c) format only 1996 Knight-Ridder Info. All rts. reserv.

01893011 72143011

A fluorescence assay for DNA with covalently linked complementary sequences.

Morgan AR; Paetkau V

Can J Biochem (CANADA) Feb 1972, 50 (2) p210-6, ISSN 0008-4018

Journal Code: CHN

Languages: ENGLISH

Document type: JOURNAL ARTICLE

16/3,AB/15 (Item 1 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

(c) 1996 American Chemical Society. All rts. reserv.

102204247 CA: 102(23)204247v PATENT

Defined sequence single strand oligonucleotides incorporating reporter groups, and nucleosides useful in such synthesis

INVENTOR(AUTHOR): Ruth, Jerry L.

LOCATION: USA

ASSIGNEE: Molecular Biosystems, Inc.

PATENT: PCT International ; WO 8403285 A1 DATE: 840830

APPLICATION: WO 84US279 (840222) \*US 468498 (830222) \*WO 83/AU254 (830222)

PAGES: 85 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C07H-017/00; C07H-019/06; C07H-015/12; C12Q-001/68 DESIGNATED COUNTRIES: AU; DK; JP; NO ; US DESIGNATED REGIONAL: CH; DE; FR; GB; NL; SE

16/3,AB/16 (Item 2 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

(c) 1996 American Chemical Society. All rts. reserv.

102109375 CA: 102(13)109375b PATENT

Assay method utilizing polynucleotide sequences  
INVENTOR(AUTHOR): Pergolizzi, Robert G.; Stavrianopoulos, Jannis G.;  
Rabbani, Elazar; Engelhardt, Dean L.; Kline, Stan  
LOCATION: USA  
ASSIGNEE: Enzo Bio Chem, Inc.  
PATENT: European Pat. Appl. ; EP 128332 A1 DATE: 841219  
APPLICATION: EP 84105028 (840504) \*US 491929 (830505)  
PAGES: 91 pp. CODEN: EPXXDW LANGUAGE: English CLASS: G01N-033/54;  
G01N-033/58; C12Q-001/68; C07G-007/00 DESIGNATED COUNTRIES: AT; BE; CH; DE  
; FR; GB; IT; LI; LU; NL; SE

16/3,AB/17 (Item 3 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

100099327 CA: 100(13)99327e JOURNAL  
Involvement of tryptophyl residues in the binding of model peptides and  
gene 32 protein from phage T4 to single-stranded polynucleotides. A  
spectroscopic method for detection of tryptophan in the vicinity of nucleic  
acid bases  
AUTHOR(S): Le Doan, Trung; Toulme, Jean Jacques; Helene, Claude  
LOCATION: Lab. Biophys., Mus. Natl. Hist. Nat., 75005, Paris, Fr.  
JOURNAL: Biochemistry DATE: 1984 VOLUME: 23 NUMBER: 6 PAGES: 1202-7  
CODEN: BICHAW ISSN: 0006-2960 LANGUAGE: English

16/3,AB/18 (Item 4 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

98055755 CA: 98(8)55755d PATENT  
Hydrophobic coating of billets  
INVENTOR(AUTHOR): Mlot-Fijalkowski, Adolf; Borrows, Kenneth P.  
LOCATION: USA  
ASSIGNEE: Magnaflux Corp.  
PATENT: Canada ; CA 1134167 A1 DATE: 821026  
APPLICATION: CA 357070 (800725) \*US 129710 (800312)  
PAGES: 9 pp. CODEN: CAXXA4 LANGUAGE: English CLASS: G01N-021/64

16/3,AB/19 (Item 5 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
(c) 1996 American Chemical Society. All rts. reserv.

87064912 CA: 87(9)64912c JOURNAL  
Fluorometric detection of deoxyribonucleic acid synthesis; possibilities

for interfacing bromodeoxyuridine dye techniques with flow fluorometry

AUTHOR(S): Latt, Samuel A.

LOCATION: Dep. Pediatr., Child. Hosp. Med. Cent., Boston, Mass.

JOURNAL: J. Histochem. Cytochem. DATE: 1977 VOLUME: 25 NUMBER: 7

PAGES: 913-26 CODEN: JHCYAS LANGUAGE: English

?

2/084,340  
12/10/96

SYSTEM:OS - DIALOG OneSearch

File 55:BIOSIS PREVIEWS(R) 1985-1996/Dec W1

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File 72:EMBASE 1985-1996/Iss 49

(c) 1996 Elsevier Science B.V.

File 76:Life Sciences Collection 1982-1996/Oct

(c) 1996 Cambridge Sci Abs

File 155:MEDLINE(R) 1966-1996/Dec W4

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\*File 155: MEDLINE updates delayed. See HELP DELAY 155.

File 399:CA SEARCH(R) 1967-1996/UD=12524

(c) 1996 American Chemical Society

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S2 211 S1 NOT PY>1984

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...examined 50 records (100)

...examined 50 records (150)

...examined 50 records (200)

...completed examining records

S3 158 RD (unique items)

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158 S3

267950 POLYMERASE

S4 33 S3 AND POLYMERASE

?T S4/3,AB/1-33

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4/3,AB/1 (Item 1 from file: 55)  
DIALOG(R)File 55:BIOSIS PREVIEWS(R)  
(c) 1996 BIOSIS. All rts. reserv.

4825450 BIOSIS Number: 79067765

MULTIPLE ORIGINS OF TRANSCRIPTION FOR THE HUMAN PLACENTAL LACTOGEN GENES  
SELVANAYAGAM C S; TASI S Y; TSIA M-J; SELVANAYAGAM P; SAUNDERS G F  
DEP. BIOCHEMISTRY AND MOLECULAR BIOLOGY, UNIV. TEXAS SYSTEM CANCER  
CENTER, M.D. ANDERSON HOSPITAL AND TUMOR INST. HOUSTON, HOUSTON, TEXAS,  
77030.

J BIOL CHEM 259 (23). 1984. 14642-14646. CODEN: JBCHA

Full Journal Title: Journal of Biological Chemistry

Language: ENGLISH

Transcriptional activity of the 3 human placental lactogen (hPL) genes was compared in vitro and their relation to the hPL RNA species obtained from term placenta was analyzed. In vitro transcription system containing the HeLa cell crude extract was used as the source for RNA polymerase II and initiation factors. Gene fragments of identical length of 0.96 kilobase pair made from hPL1, hPL3, and hPL4 each contained the 5' flanking sequence of 497 base pairs, the 1st exon, the 1st intron, and a portion of the 2nd exon. More than 90% transcripts of the hPL1 template were 470 nucleotides long, indicating that transcription was initiated at the proposed cap site. hPL3 and hPL4 genes generated heterogeneous RNA products of about 430, 470, 520 and 680 nucleotides, suggesting that multiple start points were recognized for RNA synthesis in vitro, .alpha.-Amanitin sensitivity of transcription indicated that the DNA-dependent RNA synthesis was carried out by RNA polymerase II. These results show that hPL1, hPL3, and hPL4 genes have functional promoters and multiple initiation sites for transcription. Primer extension analysis of the 5' termini of hPL RNA isolated from term placenta shows that 82-83% of the transcripts are initiated at a region 29 base pairs downstream from a "TATA" sequence. This origin is observed in vitro for the transcript 470 nucleotides long. An additional upstream initiation region (-53) accounts for 8% of transcripts in term placenta and corresponds to the origin for the in vitro transcript of 520 nucleotides. At least 3 other sites 15, 23, and 39 base pairs downstream from the major cap site are functional in vivo. The initiation site at +40 is utilized preferentially for transcription from hPL3 and hPL4 genes in vitro. The different transcription origins on hPL genes were mapped.

4/3,AB/2 (Item 2 from file: 55)  
DIALOG(R)File 55:BIOSIS PREVIEWS(R)  
(c) 1996 BIOSIS. All rts. reserv.

4815808 BIOSIS Number: 79058123

HIGH-SENSITIVITY S-1 MAPPING WITH SINGLE-STRANDED PHOSPHORUS-32-LABELED  
DNA PROBES SYNTHESIZED FROM BACTERIOPHAGE M-13MP TEMPLATES

BURKE J F

MRC CELL MUTATION UNIT, UNIV. SUSSEX, FALMER, BRIGHTON, E. SUSSEX, BN1  
9RR, UK.

GENE (AMST) 30 (1-3). 1984. 63-68. CODEN: GENED

Full Journal Title: GENE (Amsterdam)

Language: ENGLISH

A method is described by which high specific-activity single stranded (ss) [.alpha.-32P]DNA of a defined size complementary to sequences cloned into phage M13 is synthesized. The ss DNA template is annealed with a universal sequencing primer, the primer extended with DNA polymerase I Klenow fragment and the DNA duplex cut at a unique site 5' to the multiple cloning sites in the M13 phage. The reaction products are denatured and the ss .alpha.-32P probe fragment complementary to the cloned sequence is separated from the template by electrophoresis. The utility of such probes for S1 mapping is shown by mapping the 3' ends of transcripts from a mutant Drosophila heat-shock gene. The method described is up to 300 times more sensitive than conventional S1 mapping techniques.

4/3,AB/3 (Item 3 from file: 55)

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

4767557 BIOSIS Number: 79009872

BIOTIN-LABELED OLIGONUCLEOTIDES ENZYMATIC SYNTHESIS AND USE AS  
HYBRIDIZATION PROBES

MURASUGI A; WALLACE R B

DEP. MOL. GENETICS, BECKMAN RES. INST. CITY HOPE, 1450 EAST DUARTE ROAD,  
DUARTE, CALIF. 91010.

DNA (N Y) 3 (3). 1984. 269-278. CODEN: DNAAD

Full Journal Title: DNA (New York)

Language: ENGLISH

An oligonucleotide probe (23-mer) containing a single biotinylated deoxyuridine residue at the 3' terminus was prepared by a primer extension reaction using Escherichia coli DNA polymerase I (Klenow fragment). For efficient synthesis of the probe, it was necessary to add about 16-fold molar excess of the template oligonucleotide (pentadecanucleotide) to the primer oligonucleotide (nonadecanucleotide) in the reaction mixture and to continue the reaction for 2.5 h at 4.degree. C. The probe was purified by polyacrylamide gel electrophoresis under denaturing conditions. The probe could be specifically and tightly bound with avidin D in 1 M NaCl. It could be hybridized to a plasmid DNA containing a perfectly matched complementary sequence, but not to a DNA containing 5 consecutive noncomplementary bases. The hybridized biotinylated probe could be detected by avidin D and



biotinylated alkaline phosphatase, even when 1.8 ng of the plasmid DNA (0.5 fmol) was used. A general approach to the enzymatic synthesis of oligonucleotides containing a single biotinylated deoxyuridine at the 3' end is described.

4/3,AB/4 (Item 1 from file: 72)  
DIALOG(R)File 72:EMBASE  
(c) 1996 Elsevier Science B.V. All rts. reserv.

5756252 EMBASE No: 85001762

High-sensitivity S1 mapping with single-stranded (sup 3sup 2P)DNA probes synthesized from bacteriophage M13mp templates

Burke J.F.

MRC Cell Mutation Unit, University of Sussex, Falmer, Brighton, E. Sussex  
BN1 9RR UNITED KINGDOM

GENE (NETHERLANDS) , 1984, 30/1-3 (63-68) CODEN: GENED

LANGUAGES: ENGLISH

A method is described by which high-specific-activity single-stranded (ss) (alpha-sup 3sup 2P)DNA of a defined size complementary to sequences cloned into bacteriophage M13 is synthesized. The ss DNA template is annealed with a universal sequencing primer, the primer extended with DNA polymerase I Klenow fragment and the DNA duplex cut at a unique site 5' to the multiple cloning sites in the M13 phage. The reaction products are denatured and the ss alpha-sup 3sup 2P probe fragment complementary to the cloned sequence is separated from the template by electrophoresis. The utility of such probes for S1 mapping is shown by mapping the 3' ends of transcripts from a mutant Drosophila heat-shock gene. The method described here is up to 300 times more sensitive than conventional S1 mapping techniques.

4/3,AB/5 (Item 1 from file: 76)  
DIALOG(R)File 76:Life Sciences Collection  
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00772931 0772821

Selective cleavage in the avian retroviral long terminal repeat sequence by the endonuclease associated with the alpha beta form of avian reverse transcriptase.

Duyk, G.; Leis, J.; Longiaru, M.; Skalka, A.M.

Dep. Biochem., Case Western Reserve Univ. Sch. Med., Cleveland, OH 44106,  
USA

PROC. NATL. ACAD. SCI. USA. vol. 80, no. 22, pp. 6745-6749 (1983.)

DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH

SUBFILE: Biochemistry Abstracts Part 2: Nucleic Acids; Genetics Abstracts;  
Virology Abstracts

M13 recombinant DNA clones containing a 350-base sequence derived from the EcoRI fragment of two tandemly linked Rous-associated virus 2 (RAV-2) long terminal repeat (LTR) sequences have been used to map reverse transcriptase-associated endonuclease (RT-endonuclease) cleavage sites by primer extension studies. Under appropriate conditions, the alpha beta form of RT-endonuclease (composed of both the alpha and beta subunits) purified from avian sarcoma virus (Pr-C and B-77 strains) introduces a specific break in the inverted complementary repeat sequence found at the junction of the LTRs. A second site, which occurs in the lac region of the M13 vector DNA upstream from the unique EcoRI cloning site, bears no apparent sequence homology to the site at the junction of the LTRs. However, it also lies within an inverted complementary repeat and, as is the case for the site in the LTR, the break occurs to the 5' side of the axis of symmetry. Cleavage at this second site is suppressed when the vector contains the RAV-2 LTR insert. Thus, the viral LTR appears to exert a cis effect that can influence a region over 300 base pairs away.

4/3,AB/6 (Item 2 from file: 76)  
DIALOG(R)File 76:Life Sciences Collection  
(c) 1996 Cambridge Sci Abs. All rts. reserv.

00575439 0298233

Sequence Analysis of the Polymerase 1 Gene and the Secondary Structure  
Prediction of Polymerase 1 Protein of Human Influenza Virus A/WSN/33.  
Sivasubramanian, N.; Nayak, D.P.

Jonsson Comprehensive Cancer Cent., Univ. California, Los Angeles, CA  
90024, USA

J. VIROL. vol. 44, no. 1, pp. 311-320 (1982.)

DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH

SUBFILE: Virology Abstracts; Biochemistry Abstracts Part 2: Nucleic Acids;  
Genetics Abstracts; Biochemistry Abstracts Part 3: Amino Acids, Peptides  
and Proteins

The nucleotide sequence of polymerase 1 (P1) gene of a human influenza virus (A/WSN/33) has been determined by using cDNA clones, except for the last 83 nucleotides, which were obtained by primer extension. The WSN P1 gene contains 2,341 nucleotides and codes for a protein of 757 amino acids. P1 gene possesses a striking tandem repeat of 12 nucleotides (nucleotide position 2,188 to 2,199, 2,200 to 2,211) and a corresponding tandem repeat of tetrapeptide in the P1 protein. The deduced sequence of P1 protein is enriched in basic amino acids, particularly arginine. In addition, it also contains clusters of basic amino acids which may provide sites for the interaction with the template virion RNA capped primer as well as with other proteins involved in viral replication and transcription. A secondary structure prediction, using Chou and Fasman analyses, shows that the P1

protein possesses some unique features, viz., one "four-helical supersecondary structure" and four "polypeptide double helices" (antiparallel beta -pleated sheets) which are considered important in RNA binding.

4/3,AB/7 (Item 3 from file: 76)  
DIALOG(R)File 76:Life Sciences Collection  
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00567612 0273871

Specific Sequences in Native DNA That Arrest Synthesis by DNA Polymerase alpha .

Weaver, D.T.; DePamphilis, M.L.

Dep. Biol. Chem., Harvard Med. Sch., Boston, MA 02115, USA

J. BIOL. CHEM. vol. 257, no. 4, pp. 2075-2086 (1982.)

DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH

SUBFILE: Biochemistry Abstracts Part 2: Nucleic Acids; Genetics Abstracts

The effect of the DNA sequence of a template on the progress of DNA polymerase alpha was determined at the resolution of single nucleotides by using single-stranded, circular Phi X174 DNA as a template and unique Phi X174 DNA fragments terminally labeled at their 3'-ends as primers. Extension of a primer by alpha -polymerase revealed that 3'-ends of nascent DNA chains accumulated at specific arrest sites consisting of GC-rich sequences of 1-8 bases distributed nonuniformly along the template with intervening sequences of 0-140 bases. The precise location and composition of these sites were determined by DNA sequencing methods, but a consensus sequence was not detected. All arrest sites cannot be defined by secondary structure alone, although proximity to secondary structures may amplify normal variations in the rate of DNA elongation caused by primary sequences.

4/3,AB/8 (Item 4 from file: 76)  
DIALOG(R)File 76:Life Sciences Collection  
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00512627 0138297

Accessory Proteins for DNA Polymerase alpha Activity With Single-Strand DNA Templates.

Lamothe, P.; Baril, B.; Chi, A.; Lee, L.; Baril, E.

Worcester Found. Exp. Biol., Shrewsbury, MA 01545, USA

PROC. NATL. ACAD. SCI. USA. vol. 78, no. 8, pp. 4723-4727 (1981.)

DOCUMENT TYPE: Journal article LANGUAGE: ENGLISH

SUBFILE: Biochemistry Abstracts Part 3: Amino Acids, Peptides and Proteins;  
Biochemistry Abstracts Part 2: Nucleic Acids; Genetics Abstracts

Three forms of DNA polymerase alpha (DNA nucleotidyltransferase (DNA-directed), EC 2.7.7.7) were partially purified from the combined nuclear extract and postmicrosomal supernatant solution of synchronized HeLa cells. These enzymes, designated DNA polymerases alpha sub(1), alpha sub(2), and alpha sub(3), on the basis of their order of elution from DEAE-Bio-Gel, differ in their abilities to utilize single-strand DNA templates. DNA polymerase alpha sub(2) has equal catalytic activities with activated and single-strand DNAs as template-primers. DNA polymerase alpha sub(1) has only partial catalytic activity with single-strand DNA templates, and DNA polymerase alpha sub(3) is essentially inactive with this template. Successive steps of hydrophobic affinity chromatography and phosphocellulose chromatography of DNA polymerase alpha sub(2) resolved the polymerase alpha activity and two protein factors (C1 and C2) that are required for its catalytic activity with a DNA template-primer that contains extended single-strand regions. In the absence of the factors, DNA polymerase alpha activity is measurable with activated but not single-strand DNA templates. In the presence of the C1 and C2 factors DNA polymerase alpha activity with single-strand DNA templates is restored to about 75% of the catalytic activity of DNA polymerase alpha sub(2) with this template.

4/3,AB/9 (Item 1 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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05461628 85077628

High-sensitivity S1 mapping with single-stranded [32P]DNA probes synthesized from bacteriophage M13mp templates.

Burke JF

Gene (NETHERLANDS) Oct 1984, 30 (1-3) p63-8, ISSN 0378-1119

Journal Code: FOP

Languages: ENGLISH

Document type: JOURNAL ARTICLE

A method is described by which high-specific-activity single-stranded (ss) [alpha-32P]DNA of a defined size complementary to sequences cloned into bacteriophage M13 is synthesized. The ss DNA template is annealed with a universal sequencing primer, the primer extended with DNA polymerase I Klenow fragment and the DNA duplex cut at a unique site 5' to the multiple cloning sites in the M13 phage. The reaction products are denatured and the ss alpha-32P probe fragment complementary to the cloned sequence is separated from the template by electrophoresis. The utility of such probes for S1 mapping is shown by mapping the 3' ends of transcripts from a mutant Drosophila heat-shock gene. The method described here is up to 300 times more sensitive than conventional S1 mapping techniques.

4/3,AB/10 (Item 2 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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05421922 85037922

The adenovirus major late promoter TATA box and initiation site are both necessary for transcription in vitro.

Concino MF; Lee RF; Merryweather JP; Weinmann R

Nucleic Acids Res (ENGLAND) Oct 11 1984, 12 (19) p7423-33, ISSN

0305-1048 Journal Code: 08L

Contract/Grant No.: CA-09171; F32 AI-06774; CA-09171; +

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Mutagenized DNA templates and HeLa whole cell extracts were used to study the effects of promoter-specific base changes on in vitro transcription. DNA templates where the initiating adenine (+1) was changed to thymidine (AT+1) in the adenovirus 2 major late transcription unit were transcribed with 50% efficiency of the unaltered template. We have described a mutant at the TATA box, where the A at position -28 was changed to a C (AC-28). Transcription efficiency was reduced to less than 20% of control in the AC-28 mutant (Concino et al., 1983, J. Biol. Chem. 258: 8493-8496). Primer extension analysis revealed increased 5' end heterogeneity for in vitro transcripts derived from AC-28 and AT+1 DNA templates. Specific transcription was completely abolished from AT+1 DNA templates when a second change was introduced within the TATA sequence, creating a double mutant (AC-28 . AT+1). Neither the AC-28 nor the AT+1 change alone had such an effect, suggesting a coordinated interaction in transcription initiation involving both the TATA box and the initiation site.

4/3,AB/11 (Item 3 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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05373211 84297211

Variations in transcriptional activity of rDNA spacer promoters.

Morgan GT; Roan JG; Bakken AH; Reeder RH

Nucleic Acids Res (ENGLAND) Aug 10 1984, 12 (15) p6043-52, ISSN

0305-1048 Journal Code: 08L

Contract/Grant No.: GM28905

Languages: ENGLISH

Document type: JOURNAL ARTICLE

We have compared the DNA sequences of several different examples of the duplicated polymerase I promoters that are found in rDNA spacers of *Xenopus laevis*. Although different spacers exhibit different amounts of transcription in vivo, this does not seem to be due to DNA sequence

differences between spacer promoters. We have found that several different spacer promoters when subcloned and injected into oocytes exhibit similar promoter activities when transcription is assayed by primer extension analysis. Moreover, the activity of these spacer promoters is the same as that of a co-injected gene promoter. The equivalence of spacer promoter activity and gene promoter activity was also found when rDNA plasmids containing intact spacers were injected into oocytes and transcription assayed by primer extension. This is in contrast to (1) the inactivity normally exhibited by the promoters of endogenous spacers in oocytes, (2) the relative inactivity of spacer promoters found when transcription of the same rDNA plasmids is assayed by electron microscopy.

4/3,AB/12 (Item 4 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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05292498 84216498

Mapping of the cohesive overlap of duck hepatitis B virus DNA and of the site of initiation of reverse transcription.

Molnar-Kimber KL; Summers JW; Mason WS

J Virol (UNITED STATES) Jul 1984, 51 (1) p181-91, ISSN 0022-538X

Journal Code: KCV

Contract/Grant No.: AI-18641; AI-15166; CA-09035; +

Languages: ENGLISH

Document type: JOURNAL ARTICLE

The hepatitis B-like viruses have a approximately 3.2 kilobase, partially double-stranded DNA genome that is held in a circular conformation by a cohesive overlap between the 5' ends of the two strands. In addition, a protein is covalently bound to the 5' end of the minus strand of virion DNA. The sequence of the cohesive overlap region and its location relative to open reading frames and to the initiation site for minus-strand DNA synthesis, which occurs by reverse transcription of viral RNA, were investigated in duck hepatitis B virus. The 5' ends of virion DNA were mapped by restriction endonuclease analysis of labeled virion DNA, S1 nuclease digestion, and primer extension, using avian myeloblastosis virus DNA polymerase. The cohesive overlap region was shown to be 69 +/- 4 base pairs in length. It contained a 10-base pair inverted repeat in approximately the middle and a 12-base pair direct repeat near each end. The apparent initiation site of reverse transcription was determined by partial sequence analysis of dideoxynucleotide-truncated minus-strand DNA intermediates and comparison of their lengths with the length of a known DNA sequence. It mapped within two to four nucleotides of the 5' end of the minus strand of virion DNA. The results are consistent with the interpretation that the 5' end of the minus strand of virion DNA is the origin of reverse transcription and that the protein covalently bound to virion DNA is the primer of reverse transcription.

4/3,AB/13 (Item 5 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
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05108552 84032552

Complexes of Escherichia coli primase with the replication origin of G4 phage DNA.

Stayton MM; Kornberg A

J Biol Chem (UNITED STATES) Nov 10 1983, 258 (21) p13205-12, ISSN 0021-9258 Journal Code: HIV

Contract/Grant No.: GM07581

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Escherichia coli primase (dnaG protein), an essential DNA replication enzyme, synthesizes a primer at the unique origin sequence of the single-stranded circular phage G4 DNA (Rowen, L., and Kornberg, A. (1978) J. Biol. Chem. 253, 758-764). Kinetic analyses suggest that for each DNA molecule at least two primase molecules participate in the reaction. Binding of 3H-labeled primase is specific for the G4 complementary strand origin region and is saturated at approximately 2 primase molecules/DNA circle. Such complexes, isolated by gel filtration, function in the absence of additional primase to convert the phage DNA to the duplex form. Although the primase-DNA complex is stable to refiltration, the DNA-bound enzyme can dissociate and reattach to function at the origin sequence of another G4 DNA circle. An antibody to primase blocks the action of primase in the free form or within a DNA complex and even interferes with extension of the primer by DNA polymerase III holoenzyme. These kinetic and binding studies of G4 priming, the least complicated of the primase systems, suggest that 2 primase molecules form a complex at the origin region and remain bound even after transcribing a sequence to prime DNA replication.

4/3,AB/14 (Item 6 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
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05005550 83238550

Structure and sequence of the promoter area and of a 5' upstream demethylation site of the estrogen-regulated chicken vitellogenin ii gene.

Geiser M; Mattaj IW; Wilks AF; Seldran M; Jost JP

J Biol Chem (UNITED STATES) Jul 25 1983, 258 (14) p9024-30, ISSN 0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

We sequenced 487 base pairs (bp) covering the 5' end of chicken

vitellogenin II gene and 840 bp of its 5' end-flanking region. This region includes a MspI/HpaII restriction site which becomes undermethylated in chicken liver upon estrogen treatment. Southern blot analysis of restriction enzyme digests of total DNA confirms that this undermethylation site is the one situated at -611 bp from the cap sequence. This site is flanked at nucleotides -567, -629, and -667 by stretches of DNA very rich in A + T. We used S1 nuclease mapping as well as a primer extension procedure to map the transcription starting point of the vitellogenin II gene. We found a 5'CATAAAA3' box between nucleotides -32 and -26, and between nucleotides -77 and -69 a sequence (5'TTGAGAATT3') homologous to the bacterial RNA polymerase-binding site. A similar sequence (5'TGTTTACATAAAA3') is also found between nucleotides -101 and -90. A comparison of the sequence of the primer-extended DNA with the 5' end of vitellogenin II gene revealed the presence of two small exons of 53 and 21 bp between nucleotides +1 and +53, and +169 and +189, respectively, and two small introns of 115 and 100 bp between nucleotides +54 and +168, and +190 and +290, respectively. The first AUG at nucleotide +14 is in front of an open reading frame. We found that 77% of the amino acids coded by the first exon are hydrophobic, a feature compatible with a signal sequence of a secreted protein such as vitellogenin.

4/3,AB/15 (Item 7 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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05005474 83238474

The complete nucleotide sequence of the major adult beta globin gene of *Xenopus laevis*.

Patient RK; Harris R; Walmsley ME; Williams JG

J Biol Chem (UNITED STATES) Jul 25 1983, 258 (14) p8521-3, ISSN 0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

We present the complete nucleotide sequence of the major beta globin gene of *Xenopus laevis* with 127 nucleotides of sequence upstream of the gene and 212 nucleotides downstream. The start point of transcription was determined by S1 mapping and primer extension and the site of polyadenylation by comparison with the mRNA sequence determined from a cDNA clone. Comparison of the *X. laevis* sequence with other genes transcribed by RNA polymerase II reveals conserved features in the 5' flanking, 5' noncoding, intron/exon boundary, and 3' noncoding regions.

4/3,AB/16 (Item 8 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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04875904 83108904

Pure yeast RNA polymerase B (II) initiates transcription at specific points on supercoiled yeast DNA.

Lescure B

J Biol Chem (UNITED STATES) Jan 25 1983, 258 (2) p946-52, ISSN 0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Pure yeast RNA polymerase B (II) can selectively initiate abortive transcription on a supercoiled recombinant plasmid DNA carrying yeast DNA in the presence of low concentrations of ribonucleoside triphosphates and Mn<sup>2+</sup>. Five major products ranging between 60 and 150 nucleotides were characterized by hybridization. Three of them originate from the vector pBR322 and two from the yeast DNA insert. Based on a RNA primer extension reaction with recombinant M13 DNAs as template, a method allowing the mapping of the short abortive RNA products has been developed. An initiation site within the yeast DNA insert has thus precisely been mapped. The DNA sequence in this region was determined and showed several relevant features. The in vitro initiation site is preceded by a potential TATATATA box at -40 base pairs and at -105 by the sequence GTTAATCT similar to the consensus sequence GCTCAATCT usually found around 80 base pairs upstream from the cap site. Large blocks of alternated purine pyrimidine residues are found in this region as for several known yeast promoters. The 5' end of the RNA initiated from this site contains several potential signals for the initiation of translation. The possibility that a B to Z transition of DNA could be important for the interaction of the RNA polymerase with its template is discussed.

4/3,AB/17 (Item 9 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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04342741 81170741

Simian virus 40 early mRNA's in lytically infected and transformed cells contain six 5'-terminal caps.

Kahana C; Gidoni D; Canaani D; Groner Y

J Virol (UNITED STATES) Jan 1981, 37 (1) p7-16, ISSN 0022-538X  
Journal Code: KCV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Late simian virus 40 (SV40) mRNA contains eight different cap structures which we have previously identified and mapped on the viral genome. As reported here, 5'-cap heterogeneity is a common feature to both the early and the late SV40 mRNA's. methyl-3H-labeled viral mRNA was purified from cells infected at 41 degrees C with SV40 mutant tsA209. Three different cap

cores were identified: m7GpppGm, m7GpppCm, and m7GpppAm. An average of three to four m6A residues per mRNA molecule was found. RNase T2-resistant 32P-labeled early caps from tsA209-infected cells isolated and characterized. Six distinct cap I structures were identified: m7GpppCmpU (30%), m7GpppGmpC (24%), m7GpppAmpG (18%), m7GpppGmpU (13%), m7GpppGmpG (12%), and m7GpppAmpU (3%). A similar 5'-end heterogeneity was observed in early SV40 mRNA from BSC-1 cells infected with wild-type SV40 strain 777 in the presence of cytosine arabinoside and in the SV40 UV-transformed permissive line C-6. Five of these capped dinucleotides are complementary to DNA sequences at 0.66 map unit in a region previously identified by the primer extension method (Reddy et al., J. Virol. 30:279-296, 1979; Thompson et al., J. Virol. 31:437-438, 1979) as the 5' end of the early message. DNA sequences upstream from this region contain the TATTTAT (Hogness-Goldberg box), which is missing from upstream of the 5'-cap sites of late SV40 mRNA. Thus, 5'-end heterogeneity is not necessarily related to the presence or the absence of this putative transcriptional "initiation signal." When the possibility that SV40 5' caps represent transcriptional initiation sites is considered, the data also suggest that, on SV40 DNA, eucaryotic RNA polymerase II initiates transcription at multiple nucleotide sequences, including pyrimidines.

4/3,AB/18 (Item 10 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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04248596 81076596

Study of the interactions between avian myeloblastosis virus reverse transcriptase and primer tRNA. Affinity labeling and inactivation of the enzyme by periodate-treated tRNA<sup>Trp</sup>.

Araya A; Hevia E; Litvak S

Nucleic Acids Res (ENGLAND) Sep 11 1980, 8 (17) p4009-20, ISSN 0301-5610 Journal Code: O8L

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Reverse transcriptase from avian myeloblastosis virus can react with periodate-treated primer tRNA<sup>Trp</sup> (beef) to form a Schiff's base between an epsilon-NH<sub>2</sub> lysine group within the active center of the enzyme and the dialdehyde derivative of the 3' terminal ribose of tRNA. In the presence of cyanoborohydride the reversible iminium moiety of the Schiff's base is reduced to a more stable adduct. Non-primer tRNAs were not able to reduce the extent of primer fixation to the enzyme. Complete inactivation of the enzyme was attained when the ratio enzyme:tRNA in the complex was 1:1. When the 1:1 adduct was analyzed by polyacrylamide gel electrophoresis, radioactivity from the terminal adenosine of tRNA was found exclusively associated with the alpha subunit. At longer times of labeling the beta subunit was also found linked to the oxidized primer tRNA.

4/3,AB/19 (Item 11 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
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04116902 80227902

Mechanism of primer-template-dependent conversion of dNTP leads to dNMP by T5 DNA polymerase.

Das SK; Fujimura RK

J Biol Chem (UNITED STATES) Aug 10 1980, 255 (15) p7149-54, ISSN 0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

T5 DNA polymerase catalyzes both 5' leads to 3' polymerization and 3' leads to 5' hydrolysis in a processive fashion. This knowledge has been utilized to obtain evidence indicating that the enzyme has a single primer-template binding site which can function as either polymerase or exonuclease, perhaps with the cooperation of additional or different side groups. Template-dependent conversion of dNTP leads to dNMP was observed with an excess of either primer-template or enzyme. With primer-template excess, practically all the enzymes were functional as polymerase; with enzyme excess, all primer-templates were extended during the first cycle of catalysis. These observations suggest that turnover takes place at the points of chain growth. Evidence is also provided which demonstrates that the enzyme is capable of switching its direction of catalysis from 3' leads to 5' to 5' leads to 3' without leaving the primer-template. A clear correspondence between the relative amount of hydrolysis of a terminally labeled residue on the primer and the relative amount of turnover suggests that (a) the probability of hydrolysis of a given type of residue in contact with the "active site" is constant, and (b) during each turnover episode enzyme usually takes only one step in the 3' leads to 5' direction. A simple probabilistic model of turnover is discussed.

4/3,AB/20 (Item 12 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
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04071168 80182168

Transcription of simian virus 40 DNA by wheat germ RNA polymerase II. Priming of RNA synthesis by the 3'-hydroxyl of DNA at single strand nicks.

Lewis MK; Burgess RR

J Biol Chem (UNITED STATES) May 25 1980, 255 (10) p4928-36, ISSN 0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Linear simian virus 40 DNA has been transcribed in vitro with wheat germ RNA polymerase II. Transcription products have been fractionated on polyacrylamide gels and several discrete sized RNA bands are seen. The RNA band pattern is affected dramatically by deoxyribonuclease treatment during RNA isolation. This is because most of the RNA synthesized is covalently linked to DNA. This linkage has been demonstrated by density analysis in formaldehyde-CsCl gradients and by incorporation of alkali-stable ribonucleotides into DNA. The linear DNA templates transcribed were generated by treatment of circular DNA with restriction enzymes which, in addition to cutting once at a single primary site, were found also to produce single strand nicks at specific secondary sites. The discrete sized RNA bands observed result from initiation at these nicks and terminated at DNA ends. There are two modes of nick-dependent initiation. In one mode the 3'-hydroxyl terminus of the DNA at a single strand nick serves as a primer for the extension of an RNA chain. In a second mode de novo initiation of an RNA chain is promoted at the nick. RNAs which are not primed initiate predominantly with GTP. The catalytic action of wheat germ RNA polymerase II is similar to that of Escherichia coli core RNA polymerase which has also been shown to synthesize primarily RNA which is covalently linked to DNA.

4/3,AB/21 (Item 13 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
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03898451 80009451

Characterization of the 5'-terminal structure of simian virus 40 early mRNA's.

Thompson JA; Radonovich MF; Salzman NP

J Virol (UNITED STATES) Aug 1979, 31 (2) p437-46, ISSN 0022-538X

Journal Code: KCV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

RPC-5 reverse-phase chromatography has been used to isolate fragments of simian virus 40 DNA generated by appropriate digestions with restriction endonucleases. Ten specific DNA fragments, mapping successively in a counterclock-wise direction from 0.67 to 0.515 on the simian virus 40 genome, were each hybridized to cytoplasmic mRNA obtained during the early phase of simian virus 40 infection. Primer extension methods with reverse transcriptase were used to characterize the 5' ends of two species of viral mRNA which were fractionated on sucrose gradients. Analysis of the complementary DNA products demonstrated the presence of two different spliced structures of simian virus 40 early mRNA's, both of which had the same 5'-end sequences (AUU), located at residues 18 to 20 on the viral genome. The mRNA for small-t contained a segment 588 bases in length (residues 18 to 605) spliced to residues 672. A 66-nucleotide segment rich

in adenine-thymine was spliced out of this mRNA. The mRNA for large-T contained a segment 308 bases in length (residues 18 to 325) which is also spliced to residue 672. A 346-base segment was spliced from this mRNA. The results suggest that there are two levels for control of genetic expression. One would be the regulation of initiation of transcription at a common promoter; the other involves post-transcriptional splicing.

4/3,AB/22 (Item 14 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
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03862366 79239366

The effect of template secondary structure on vaccinia DNA polymerase.  
Challberg MD; Englund PT  
J Biol Chem (UNITED STATES) Aug 25 1979, 254 (16) p7820-6, ISSN  
0021-9258 Journal Code: HIV  
Languages: ENGLISH  
Document type: JOURNAL ARTICLE

Vaccinia virus DNA polymerase will utilize a substrate consisting of phi X174 DNA primed with a strand of a unique restriction fragment, but the reaction is inefficient. Examination of the reaction products by alkaline agarose gel electrophoresis revealed a few discrete fragments, each corresponding to an extended primer strand. This result implies that specific barriers exist on the phi X174 template which impede, but do not completely halt, the progress of the enzyme. Only a few per cent of the template molecules were completely copied. Similar findings were reported by Sherman and Gefter using Escherichia coli DNA polymerase II and fd DNA (J. Mol. Biol. (1976) 103, 61-76). Several observations suggest that the barriers are regions of template secondary structure. Some barriers are more effective than others, and they increase in both effectiveness and number as the temperature is decreased. The same barriers are observed with T4 DNA polymerase, but none are detected with E. coli DNA polymerase I. Finally, the major barriers are located in regions of the phi X174 sequence known to contain hairpin structures of relatively high stability. The exact stopping point of one of the major barriers is within the duplex stem of a hairpin structure. These results show that DNA polymerases are a useful probe of the secondary structure of a single-stranded DNA.

4/3,AB/23 (Item 15 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
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03628696 79005696

Inhibition of primase, the dnaG protein of Escherichia coli by 2'-deoxy-2'-azidocytidine triphosphate.

Reichard P; Rowen L; Eliasson R; Hobbs J; Eckstein F  
J Biol Chem (UNITED STATES) Oct 10 1978, 253 (19) p7011-6, ISSN  
0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2'-Deoxy-2'-azidocytidine-5'-triphosphate was investigated as an inhibitor in two reconstructed enzyme systems which catalyze the replication of two viral DNAs. During replication of the duplex replicative form of phiX174 DNA, DNA polymerase III holoenzyme was weakly inhibited and inhibition was reversed by dCTP. A more pronounced inhibition, not reversed by either dCTP or CTP, was observed during replication of the single-stranded DNA of the bacteriophage G4, a close relative of phiX174. This effect depended on the incorporation of 2'-deoxy-2'-azidocytidine-5'-triphosphate by primase (dnaG protein) which synthesizes a 29-residue RNA primer at the unique origin of bacteriophage G4 DNA replication. Extension of the primer strand, terminated by 2'-deoxy-2'-azidocytidine-5'-triphosphate is then severely inhibited. Primase was also inhibited by the 2'-deoxy-2'-azido derivatives of ATP, GTP, and UTP.

4/3,AB/24 (Item 16 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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03516963 78150963

A multienzyme system for priming the replication of phiX174 viral DNA.

McMacken R; Kornberg A

J Biol Chem (UNITED STATES) May 10 1978, 253 (9) p3313-9, ISSN  
0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Synthesis of the oligonucleotides that prime replication of phiX174 single-stranded DNA employs complex protein machinery of the host cell which is probably used by the cell to replicate its own chromosome. Primer synthesis depends on at least five proteins (DNA binding protein, dnaB and dnaC proteins, protein i, and protein n) and ATP to form a replication intermediate and another protein, primase (dnaG protein), to assemble the oligonucleotide by template transcription. The data in this paper show that ribo- and deoxyribonucleoside triphosphates can serve as substrates and form hybrid primers when present together. Both RNA and DNA primers were initiated with ATP. At least three of the four base-pairing nucleoside triphosphates were required for the transcription that generates effective primers. Over 90% of the RNA and DNA transcripts were extended into complementary strands by DNA polymerase III holoenzyme. At optimal triphosphate concentrations, the rate and extent of primer formation were greater from ribonucleoside triphosphates than from deoxyribonucleoside triphosphates. Uncoupled from DNA replication, the length of RNA primers

was 14 to 50 residues, the DNA primers 4 to 20 residues. The fingerprint pattern of an RNase digest of RNA primers has a complexity suggestive of transcription from many sites on the phiX174 template. The multienzyme priming system is highly specific for phiX174 DNA as template.

4/3,AB/25 (Item 17 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
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03459856 78093856

Role of bacteriophage T7 DNA primase in the initiation of DNA strand synthesis.

Scherzinger E; Lanka E; Hillenbrand G

Nucleic Acids Res (ENGLAND) Dec 1977, 4 (12) p4151-63, ISSN 0301-5610  
Journal Code: O8L

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Bacteriophage T7 DNA primase (gene-4 protein, 66,000 daltons) enables T7 DNA polymerase to initiate the synthesis of DNA chains on single-stranded templates. An initial step in the process of chain initiation is the formation of an oligoribonucleotide primer by T7 primase. The enzyme, in the presence of natural SS DNA, Mg++ (or Mn++), ATP and CTP (or a mixture of all 4 rNTPs), catalyzes the synthesis of di-, tri-, and tetra-ribonucleotides all starting at the 5' terminus with pppA. In a subsequent step requiring both T7 DNA polymerase and primase, the short oligoribonucleotides (predominantly pppA-C-C-AOH) are extended by covalent addition of deoxyribonucleotides. With the aid of primase, T7 DNA polymerase can also utilize efficiently a variety of synthetic tri-, tetra-, or pentanucleotides as chain initiators. T7 primase apparently plays an active role in primer extension by stabilizing the short primer segments in a duplex state on the template DNA.

4/3,AB/26 (Item 18 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
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03266408 77168408

New procedure for the direct analysis of in vitro reverse transcription of Rous sarcoma virus RNA.

Darlix JL; Bromley PA; Spahr PF

J Virol (UNITED STATES) Apr 1977, 22 (1) p118-29, ISSN 0022-538X  
Journal Code: KCV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Based on the observation that in vitro transcription of Rous sarcoma

virus (RSV) RNA by avian myeloblastosis virus DNA polymerase renders the RNA PROGRESSIVELY MORE SENSITIVE TO Escherichia coli RNase H digestion, a new procedure for the in situ analysis of this process has been developed. In vitro transcription products of 32P-labeled RSV RNA are first treated with RNase H, the resistant fraction is then digested to completion with RNase T1, and the oligonucleotides are analyzed by a fingerprint technique. By using the established order of these oligonucleotides along the RNA molecule, a comparison of the yields of each oligonucleotide, before and after transcription, allows qualitative and quantitative in situ analyses of the transcription process. Using this new procedure, we find that upon transcription of purified RSV RNA, DNA synthesis occurs mainly at three sites, one near the 5' end and two near the center of the subunit RNA molecule, and that most of these RNA molecules are competent templates for limited transcription at these specific sites. We also show that purified RSV 70S RNA contains a low-molecular-weight DNA hybridized to a nucleotide sequence near the center of the subunit molecule. Furthermore, we find that the low-molecular-weight nucleic acid fraction extracted from purified RSV virions contains DNA that can hybridize to RSV 70S RNA and that the virion DNA in such hybrids can function as a primer for an extensive in vitro reverse transcription.

4/3,AB/27 (Item 19 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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03255850 77157850

Chemical synthesis of an octanucleotide complementary to a portion of the cohesive end of P2 DNA and studies on the stability of duplex formation with P2 DNA.

Padmanabhan R

Biochemistry (UNITED STATES) May 3 1977, 16 (9) p1996-2003, ISSN 0006-2960 Journal Code: A0G

Languages: ENGLISH

Document type: JOURNAL ARTICLE

A pyrimidine octanucleotide complementary to one of the cohesive ends of P2 DNA was chemically synthesized. Its sequence, d(C-T-T-T-C-C-C-C-OH), was verified by labeling it at the 5' end, followed by partial enzyme digestion and separation by a two-dimensional fingerprinting system. A single ribo-G residue was added to its 3' end using calf thymus deoxynucleotidyl terminal transferase. The resulting nonanucleotide primer was used in a detailed study on the stability of the duplexes formed in the partial as well as complete repair synthesis catalyzed by DNA polymerase I, at 5 degrees C in the presence of 70 mM potassium phosphate and 70 mM NaCl. The nonanucleotide primer was able to form a stable duplex with P2 DNA template only in the presence of DNA polymerase I. When the chain lengths of pyrimidine oligonucleotides were varied from 4 to 8 to test their abilities



to serve as primers for the enzymatic repair synthesis, it was revealed that the minimum length required for the primer function is 8. Using the nonanucleotide as the primer and the right-hand cohesive end of the DNA as the template, repair synthesis was initiated simultaneously at the 3' end of the primer as well as at the right-hand 3' end of the DNA. This resulted in a decrease in the efficiency of repair synthesis at the 3' end of the primer, possibly due to the displacement of the primer by the enzyme. The enzyme was unable to displace the primer, when the primer was extended to a 13-mer prior to the initiation of repair synthesis at the 3'-OH end of the DNA. These data suggest that the strand displacement by DNA polymerase I at 5 degrees C in the presence of 70 mM potassium phosphate and 70 mM NaCl is not significant when the duplex is at least 13 nucleotides long. The efficiency of the repair synthesis at the 3'-OH end of the DNA-primer duplex could be increased by blocking the repair synthesis at the 3'-OH end of the DNA by converting it to 3'-phosphate. This method could be useful in DNA sequence analysis, where such specific repair synthesis is desired.

4/3,AB/28 (Item 20 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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03084187 76265187

Nucleotide sequence that binds primer for DNA synthesis to the avian sarcoma virus genome.

Cordell B; Stavnezer E; Friedrich R; Bishop JM; Goodman HM

J Virol (UNITED STATES) Aug 1976, 19 (2) p548-58, ISSN 0022-538X

Journal Code: KCV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Initiation of transcription from the genome of avian sarcoma virus by RNA-directed DNA polymerase in vitro requires tRNA<sup>trp</sup> as a primer. The tRNA is bound to the viral genome by a sequence of 16 contiguous nucleotides (U-C-A-C-G-U-C-G-G-G-U-C-A-C-Cp), beginning with the penultimate base at the 3' terminus of the primer and extending through the acceptor stem into loop IV of the tRNA. Consequently, the native conformation of the tRNA must be disrupted by the binding of primer to the viral genome. The binding sequence does not include two adjacent residues of pseudouridine in loop IV, which distinguish the primer from many other tRNAs, and the 3' terminal adenosine of primer may also be excluded from base pairing with the viral genome.

4/3,AB/29 (Item 21 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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03079248 76260248

Control of mutation frequency by bacteriophage T4 DNA polymerase. I. The CB120 antimutator DNA polymerase is defective in strand displacement.

Gillin FD; Nossal NG

J Biol Chem (UNITED STATES) Sep 10 1976, 251 (17) p5219-24, ISSN 0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

The ts CB1200 (antimutator) mutation in bacteriophage T4 DNA polymerase increases the accuracy of DNA replication since it results in a decrease in the frequency of mutations in other phage genes. The CB120 polymerase differs from the wild type enzyme in the slow rate at which it copies templates where primer extension requires displacement of polynucleotides base-paired to the template strand, even in the presence of the T4 DNA unwinding protein (gene 32-protein). The ratio of nucleotides turned over (DNA-dependent conversion of deoxynucleoside triphosphate to deoxynucleoside monophosphate) to nucleotides stably incorporated into product is 10 to 100 times higher with the mutant than wild type enzyme, depending on the DNA used as the template. This high turnover rate may increase the efficiency of removal of noncomplementary nucleotides by the antimutator enzyme and is in agreement with the findings of Muzyczka et al, (Muzyczka, N., Poland, R. L., and Bessman, M. J. (1972) J. Biol. Chem. 247, 7116-7122) with the L141 and L42 antimutator T4 DNA polymerases. Since the 3'- to 5'-exonuclease activity of the CB120 mutant polymerase is not higher than that of the wild type enzyme, it is suggested that the high turnover rate may result from increased opportunity to remove newly incorporated nucleotides due to the slow rate at which the mutant enzyme moves to the next template nucleotide. In the accompanying paper we show that the CB120 antimutator polymerase also initially selects incorrect nucleotides for incorporation less frequently than the wild type enzyme. Thus this antimutator polymerase appears to have both greater accuracy in nucleotide selection and an enhanced ability to remove incorrect nucleotides.

4/3,AB/30 (Item 22 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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02865291 76046291

Relaxation complexes of poasmid DNA and protein. III. Association of protein with the 5' terminus of the broken DNA strand in the relaxed complex of plasmid ColE1.

Guiney DG; Helinski DR

J Biol Chem (UNITED STATES) Nov 25 1975, 250 (22) p8796-803, ISSN 0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

The location of the protein in the open circular DNA form of the ColE1 DNA-protein relaxation complex, induced by treatment with sodium dodecyl sulfate, has been studied using several enzymes of DNA metabolism. *Escherichia coli* exonucleases I and III are able to degrade extensively the nicked strand of the relaxed complex from the 3' end. DNA polymerase I can initiate synthesis using the relaxed complex as template-primer and specifically extends the 3' end of the nicked strand. The 5' end of the sodium dodecyl sulfate-relaxed complex, however, is blocked to the 5'-3' hydrolytic action T7 exonuclease. This block remains after trypsin treatment of the sodium dodecyl sulfate-relaxed complex but is removed by Pronase treatment. T4 DNA ligase is unable to seal either the sodium dodecyl sulfate-relaxed complex or the Pronase-treated relaxed complex even after pretreatment of the relaxed complex with T4 DNA polymerase and polynucleotide kinase. However, pretreatment with DNA polymerase I and the four deoxyribonucleoside triphosphates facilitates ligase closure of the Pronase-treated relaxed complex but not the sodium dodecyl sulfate-relaxed complex. These studies indicate that the protein in the relaxed ColE1 complex is located at or near the 5' end of the nicked strand.

4/3,AB/31 (Item 23 from file: 155)  
DIALOG(R) File 155:MEDLINE(R)  
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02804343 75211343

dnaG gene product, a rifampicin-resistant RNA polymerase, initiates the conversion of a single-stranded coliphage DNA to its duplex replicative form.

Bouche JP; Zechel K; Kornberg A  
J Biol Chem (UNITED STATES) Aug 10 1975, 250 (15) p5995-6001, ISSN 0021-9258 Journal Code: HIV  
Languages: ENGLISH  
Document type: JOURNAL ARTICLE

The protein responsible for the initiation of conversion of single-stranded phage G4 DNA to the duplex replicative form has been purified approximately 3000-fold and identified with *Escherichia coli* dnaG gene product. The protein is a rifampicin-resistant RNA polymerase of approximately 64,000 daltons. It catalyzes the incorporation of the four ribonucleoside triphosphates into an oligoribonucleotide, using as template the single-stranded DNA coated with the DNA unwinding protein of *E. coli*. An RNA transcript of a unique region of the chromosome can serve as a primer by covalent extension by DNA polymerase III holoenzyme to form a nearly full-length linear complementary strand. A similar role for the dnaG protein in the initiation of nascent (Okazaki) fragments in replication of the host chromosome is discussed.

4/3,AB/32 (Item 24 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)  
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02782421 75189421

DNA sequence analysis. Terminal sequences of bacteriophage phi80.

Bambara R; Wu R

J Biol Chem (UNITED STATES) Jun 25 1975, 250 (12) p4607-18, ISSN  
0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Sequences of the cohesive ends and the 3'-terminal regions of phi80 DNA have been determined. Sequences of the cohesive ends were obtained through the use of two standard methods. The first method involved the incorporation of all four labeled deoxyribonucleotides into the phi80 cohesive ends using DNA polymerase I. The DNA was then partially digested with micrococcal nuclease or pancreatic DNase. The products were separated by two-dimensional electrophoresis and characterized by composition, 3'-terminal, and nearest neighbor analyses. The second method involved partial incorporation using one, two, or three labeled deoxyribonucleotides followed by similar analyses. Sequences of the double-stranded regions adjacent to the cohesive ends were determined by three new methods. These methods were: (a) the DNA was specifically labeled at the 3' terminus and then partially degraded. Labeled oligonucleotide products were sequenced by their mobilities on various separation systems. (b) The cohesive ends were enlarged by limited degradation with exonuclease III. After this treatment, the DNA was partially repaired with labeled nucleotides, digested, and the products were analyzed. (c) A synthetic oligonucleotide primer was bound to phi80 DNA which had been repaired with DNA polymerase I, and then partially digested with lambda-exonuclease. The primer was extended into the region of interest by partial repair with labeled nucleotides. The extended primer was isolated and analyzed.

4/3,AB/33 (Item 1 from file: 399)  
DIALOG(R)File 399:CA SEARCH(R)  
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94203971 CA: 94(25)203971f JOURNAL

Addition of deoxynucleotides to an RNA primer by a DNA polymerase in human platelets

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JOURNAL: Biochem. Biophys. Res. Commun. DATE: 1981 VOLUME: 99 NUMBER:  
4 PAGES: 1191-8 CODEN: BBRCA9 ISSN: 0006-291X LANGUAGE: English  
?PAUSE